

CB

PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/868,604

DATE: 07/05/2001

TIME: 16:16:16

Input Set : A:\Seqlist.txt

Output Set: N:\CRF3\07032001\I868604.raw

ENTERED

```

3 <110> APPLICANT: Alex Bollen
4     Alain Fauconnier
5     Edmond Godfroid
7 <120> TITLE OF INVENTION; Vaccine
10 <130> FILE REFERENCE: B45168
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/868,604
C--> 12 <141> CURRENT FILING DATE: 2001-06-20
12 <160> NUMBER OF SEQ ID NOS: 82
14 <170> SOFTWARE: FastSEQ for Windows Version 3.0
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 2100
18 <212> TYPE: DNA
19 <213> ORGANISM: Bordetella pertussis
21 <220> FEATURE:
22 <221> NAME/KEY: CDS
23 <222> LOCATION: (1)...(2100)
25 <400> SEQUENCE: 1
26  atg acg agc aag aaa tcc att cgc cgc ctg caa cgc gcg gtg gcg ctg      48
27  Met Thr Ser Lys Lys Ser Ile Arg Arg Leu Gln Arg Ala Val Ala Leu
28  1          5          10          15
30  gcc acc agc cgc aac gac atc gta ctg gcc gtg ctc atc gtg gcg atc      96
31  Ala Thr Ser Arg Asn Asp Ile Val Leu Ala Val Leu Ile Val Ala Ile
32  20          25          30
34  gtc ttc atg atg atc ctg ccg ttg ccc aca acg ctg gtc gac gtg ctg      144
35  Val Phe Met Met Ile Leu Pro Leu Pro Thr Thr Leu Val Asp Val Leu
36  35          40          45
38  atc ggt gcg aac atg acg ctg tcg gca gtc ctg ctg atg gtc gcg atg      192
39  Ile Gly Ala Asn Met Thr Leu Ser Ala Val Leu Leu Met Val Ala Met
40  50          55          60
42  tac ctg cct tcg ccc ctg gcg ttt tcc tcg ttc cct tcg gtc ctg ctg      240
43  Tyr Leu Pro Ser Pro Leu Ala Phe Ser Ser Phe Pro Ser Val Leu Leu
44  65          70          75          80
46  gtc acc acg ctg ttc cgg ctg ggc atc tcc atc gcg acc acg cgg ctg      288
47  Val Thr Thr Leu Phe Arg Leu Gly Ile Ser Ile Ala Thr Thr Arg Leu
48  85          90          95
50  atc ctg ctg caa ggc gat gcc ggc cac atc atc gag acc ttc ggc aac      336
51  Ile Leu Leu Gln Gly Asp Ala Gly His Ile Ile Glu Thr Phe Gly Asn
52  100         105         110
54  ttc gtg gtg ggc ggc aac ctg atc gtc ggc ctg gtg gtt ttc ctc atc      384
55  Phe Val Val Gly Gly Asn Leu Ile Val Gly Leu Val Val Phe Leu Ile
56  115         120         125
58  ctc acg atc gtg cag ttc gtg gtc atc acc aaa ggc gcg gag cgg gtg      432
59  Leu Thr Ile Val Gln Phe Val Val Ile Thr Lys Gly Ala Glu Arg Val
60  130         135         140
62  gcc gaa gtc gcc gcg cgc ttc tcg ctg gac gcc atg ccc ggc aag cag      480
63  Ala Glu Val Ala Ala Arg Phe Ser Leu Asp Ala Met Pro Gly Lys Gln
64  145         150         155         160

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66	atg tcc atc gac gcg gac ttg cgc gcg ggc acc ata gac atg gac gaa	528
67	Met Ser Ile Asp Ala Asp Leu Arg Ala Gly Thr Ile Asp Met Asp Glu	
68	165 170 175	
70	gcc cga cgc cga cgc cgt acg gtc gag aag gaa agc caa ctg tat ggc	576
71	Ala Arg Arg Arg Arg Arg Thr Val Glu Lys Glu Ser Gln Leu Tyr Gly	
72	180 185 190	
74	gcc atg gac ggc gcg atg aag ttc gtc aag ggc gat gcc atc gcc ggc	624
75	Ala Met Asp Gly Ala Met Lys Phe Val Lys Gly Asp Ala Ile Ala Gly	
76	195 200 205	
78	ctg atc atc gtt gcc gtc aac ctg ctt ggc ggc atg ctg gtc ggc gtg	672
79	Leu Ile Ile Val Ala Val Asn Leu Leu Gly Gly Met Leu Val Gly Val	
80	210 215 220	
82	ctg cag cgc ggc ctg agc gcc ggc gag gcc gtg cag aca tat gcc atc	720
83	Leu Gln Arg Gly Leu Ser Ala Gly Glu Ala Val Gln Thr Tyr Ala Ile	
84	225 230 235 240	
86	ctg acc ata ggc gac ggg ctc atc gcg cag atc ccg gcg ctg ttc atc	768
87	Leu Thr Ile Gly Asp Gly Leu Ile Ala Gln Ile Pro Ala Leu Phe Ile	
88	245 250 255	
90	gcc atc tgc gcc gga atc atc gtg acg cgg gtg cag acc ggg gat ggc	816
91	Ala Ile Cys Ala Gly Ile Ile Val Thr Arg Val Gln Thr Gly Asp Gly	
92	260 265 270	
94	ccc tcc aac gta ggc acc gac atc gcc gca caa gtg ctg gcg cag cct	864
95	Pro Ser Asn Val Gly Thr Asp Ile Gly Ala Gln Val Leu Ala Gln Pro	
96	275 280 285	
98	cgc gcc ctg gtc att gcc ggc gcg atc tcg gca ggc ctg ggc ctc att	912
99	Arg Ala Leu Val Ile Ala Gly Ala Ile Ser Ala Gly Leu Gly Leu Ile	
100	290 295 300	
102	ccc ggc atg ccc acg ctg gtc ttc ttc gcc ctg gcc gcc gcg gtg ggc	960
103	Pro Gly Met Pro Thr Leu Val Phe Phe Ala Leu Ala Ala Ala Val Gly	
104	305 310 315 320	
106	acc atc ggt ttc gta ctg ctg cgc gca tcc cag cgt ccg ccc gaa ggc	1008
107	Thr Ile Gly Phe Val Leu Leu Arg Ala Ser Gln Arg Pro Pro Glu Gly	
108	325 330 335	
110	gcc gag ccc gcg ctc gcc ggc atg gct gcc gac ggc cag ccc cgc acc	1056
111	Ala Glu Pro Ala Leu Ala Gly Met ala Ala Asp Gly Gln Pro Arg Thr	
112	340 345 350	
114	cgc gcg ccg gcg gat ggg cag gcg gaa ttc gcc ccc acc gtc ccg ctg	1104
115	Arg Ala Pro Ala Asp Gly Gln Ala Glu Phe Ala Pro Thr Val Pro Leu	
116	355 360 365	
118	atc atc gac gta gcc gcg cgg ctg cag ccc cgg ttc gag ccg gcc acc	1152
119	Ile Ile Asp Val Ala Ala Arg Leu Gln Pro Arg Phe Glu Pro Ala Thr	
120	370 375 380	
122	ctc acc gac gat ctg ctg cag atc cgg cgg gcg ctc tat ttc gac ctg	1200
123	Leu Thr Asp Asp Leu Leu Gln Ile Arg Arg Ala Leu Tyr Phe Asp Leu	
124	385 390 395 400	
126	ggc gtg ccg ttt ccc gcc atc cag ttg cgc ttc acc gaa gcg ctg gcc	1248
127	Gly Val Pro Phe Pro Gly Ile Gln Leu Arg Phe Thr Glu Ala Leu Ala	
128	405 410 415	
130	gcc aat acc tac acc atc gtg ctg tcg gag atc ccg gtg gcg caa gga	1296

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131	Ala Asn Thr Tyr Thr Ile Val Leu Ser Glu Ile Pro Val Ala Gln Gly	
132	420 425 430	
134	atg ttg cgc gac gat gcc gtg ctg gtg cgg gac acc gag cag aac ctg	1344
135	Met Leu Arg Asp Asp Ala Val Leu Val Arg Asp Thr Glu Gln Asn Leu	
136	435 440 445	
138	cag gcc ctg cgg atc gca tac gaa acg ggc gcg gcc ttt ctg ccc gat	1392
139	Gln Ala Leu Arg Ile Ala Tyr Glu Thr Gly Ala Ala Phe Leu Pro Asp	
140	450 455 460	
142	acg ccc acg atc tgg gtt gcg gcc agt ctg acc ggc gcc ttg cgc gat	1440
143	Thr Pro Thr Ile Trp Val Ala Ala Ser Leu Thr Gly Ala Leu Arg Asp	
144	465 470 475 480	
146	gca ggt att cct tac ctg ggt atc agc cag atc ctg act tgg cac ttg	1488
147	Ala Gly Ile Pro Tyr Leu Gly Ile Ser Gln Ile Leu Thr Trp His Leu	
148	485 490 495	
150	gca tat gta ttg aaa aaa tat tca gcc gat ttc atc ggc atc cag gaa	1536
151	Ala Tyr Val Leu Lys Lys Tyr Ser Ala Asp Phe Ile Gly Ile Gln Glu	
152	500 505 510	
154	acc cgg ttt ctg ctt tcg gcc atg gaa gaa cga ttt ccc gat ctg gtc	1584
155	Thr Arg Phe Leu Leu Ser Ala Met Glu Glu Arg Phe Pro Asp Leu Val	
156	515 520 525	
158	aag gag tgc ctg cgc gtc atg ccg gtg cag aag att gcc gaa atc ctg	1632
159	Lys Glu Cys Leu Arg Val Met Pro Val Gln Lys Ile Ala Glu Ile Leu	
160	530 535 540	
162	cag cgc ctt gtt tcc gaa gaa gtg tcg ata cgc aac ctg cgc gcc gtc	1680
163	Gln Arg Leu Val Ser Glu Glu Val Ser Ile Arg Asn Leu Arg Ala Val	
164	545 550 555 560	
166	ctg gaa gcg ctg gtc gaa tgg ggc cag aag gaa aag gat acc gtc ctg	1728
167	Leu Glu Ala Leu Val Glu Trp Gly Gln Lys Glu Lys Asp Thr Val Leu	
168	565 570 575	
170	ctt acg gag tat gtc cga atc gca ctc aag cgc tat atc agc cac aag	1776
171	Leu Thr Glu Tyr Val Arg Ile Ala Leu Lys Arg Tyr Ile Ser His Lys	
172	580 585 590	
174	tac acc agc ggc cac aat atc ctg ccc gcc tac ctg ctg gcc ccc aag	1824
175	Tyr Thr Ser Gly His Asn Ile Leu Pro Ala Tyr Leu Leu Ala Pro Lys	
176	595 600 605	
178	gtc gag gaa acc gtg cgc gcc gcc atc cgg cag acc gcc gcc ggc agt	1872
179	Val Glu Glu Thr Val Arg Ala Ala Ile Arg Gln Thr Ala Ala Gly Ser	
180	610 615 620	
182	tat ctc gcc ctc gat ccg gac acg aca cgc cga ctg gtc gag cac atc	1920
183	Tyr Leu Ala Leu Asp Pro Asp Thr Thr Arg Arg Leu Val Glu His Ile	
184	625 630 635 640	
186	cgt caa tgt gtc ggc gat ctg gcc gcc ggc gcg agc cgt ccc gtc ttg	1968
187	Arg Gln Cys Val Gly Asp Leu Ala Ala Gly Ala Ser Arg Pro Val Leu	
188	645 650 655	
190	ctg acg tcg atg gac atc cgg cgc tac acg cgc aag atg ata gaa gcc	2016
191	Leu Thr Ser Met Asp Ile Arg Arg Tyr Thr Arg Lys Met Ile Glu Ala	
192	660 665 670	
194	gat ctc tac gcc ctg ccg gtg ctg tcc tac cag gaa ctg acg ccg gag	2064
195	Asp Leu Tyr Ala Leu Pro Val Leu Ser Tyr Gln Glu Leu Thr Pro Glu	

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196          675          680          685
198 atc aat gta cag ccc ctg ggc agg gtg gat cta tga          2100
199 Ile Asn Val Gln Pro Leu Gly Arg Val Asp Leu *
200          690          695
203 <210> SEQ ID NO: 2
204 <211> LENGTH: 699
205 <212> TYPE: PRT
206 <213> ORGANISM: Bordetella pertussis
208 <400> SEQUENCE: 2
209 Met Thr Ser Lys Lys Ser Ile Arg Arg Leu Gln Arg Ala Val Ala Leu
210 1 5 10 15
211 Ala Thr Ser Arg Asn Asp Ile Val Leu Ala Val Leu Ile Val Ala Ile
212 20 25 30
213 Val Phe Met Met Ile Leu Pro Leu Pro Thr Thr Leu Val Asp Val Leu
214 35 40 45
215 Ile Gly Ala Asn Met Thr Leu Ser Ala Val Leu Leu Met Val Ala Met
216 50 55 60
217 Tyr Leu Pro Ser Pro Leu Ala Phe Ser Ser Phe Pro Ser Val Leu Leu
218 65 70 75 80
219 Val Thr Thr Leu Phe Arg Leu Gly Ile Ser Ile Ala Thr Thr Arg Leu
220 85 90 95
221 Ile Leu Leu Gln Gly Asp Ala Gly His Ile Ile Glu Thr Phe Gly Asn
222 100 105 110
223 Phe Val Val Gly Gly Asn Leu Ile Val Gly Leu Val Val Phe Leu Ile
224 115 120 125
225 Leu Thr Ile Val Gln Phe Val Val Ile Thr Lys Gly Ala Glu Arg Val
226 130 135 140
227 Ala Glu Val Ala Ala Arg Phe Ser Leu Asp Ala Met Pro Gly Lys Gln
228 145 150 155 160
229 Met Ser Ile Asp Ala Asp Leu Arg Ala Gly Thr Ile Asp Met Asp Glu
230 165 170 175
231 Ala Arg Arg Arg Arg Arg Thr Val Glu Lys Glu Ser Gln Leu Tyr Gly
232 180 185 190
233 Ala Met Asp Gly Ala Met Lys Phe Val Lys Gly Asp Ala Ile Ala Gly
234 195 200 205
235 Leu Ile Ile Val Ala Val Asn Leu Leu Gly Gly Met Leu Val Gly Val
236 210 215 220
237 Leu Gln Arg Gly Leu Ser Ala Gly Glu Ala Val Gln Thr Tyr Ala Ile
238 225 230 235 240
239 Leu Thr Ile Gly Asp Gly Leu Ile Ala Gln Ile Pro Ala Leu Phe Ile
240 245 250 255
241 Ala Ile Cys Ala Gly Ile Ile Val Thr Arg Val Gln Thr Gly Asp Gly
242 260 265 270
243 Pro Ser Asn Val Gly Thr Asp Ile Gly Ala Gln Val Leu Ala Gln Pro
244 275 280 285
245 Arg Ala Leu Val Ile Ala Gly Ala Ile Ser Ala Gly Leu Gly Leu Ile
246 290 295 300
247 Pro Gly Met Pro Thr Leu Val Phe Phe Ala Leu Ala Ala Val Gly
248 305 310 315 320

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```

249 Thr Ile Gly Phe Val Leu Leu Arg Ala Ser Gln Arg Pro Pro Glu Gly
250           325           330           335
251 Ala Glu Pro Ala Leu Ala Gly Met ala Ala Asp Gly Gln Pro Arg Thr
252           340           345           350
253 Arg Ala Pro Ala Asp Gly Gln Ala Glu Phe Ala Pro Thr Val Pro Leu
254           355           360           365
255 Ile Ile Asp Val Ala Ala Arg Leu Gln Pro Arg Phe Glu Pro Ala Thr
256           370           375           380
257 Leu Thr Asp Asp Leu Leu Gln Ile Arg Arg Ala Leu Tyr Phe Asp Leu
258           385           390           395           400
259 Gly Val Pro Phe Pro Gly Ile Gln Leu Arg Phe Thr Glu Ala Leu Ala
260           405           410           415
261 Ala Asn Thr Tyr Thr Ile Val Leu Ser Glu Ile Pro Val Ala Gln Gly
262           420           425           430
263 Met Leu Arg Asp Asp Ala Val Leu Val Arg Asp Thr Glu Gln Asn Leu
264           435           440           445
265 Gln Ala Leu Arg Ile Ala Tyr Glu Thr Gly Ala Ala Phe Leu Pro Asp
266           450           455           460
267 Thr Pro Thr Ile Trp Val Ala Ala Ser Leu Thr Gly Ala Leu Arg Asp
268           465           470           475           480
269 Ala Gly Ile Pro Tyr Leu Gly Ile Ser Gln Ile Leu Thr Trp His Leu
270           485           490           495
271 Ala Tyr Val Leu Lys Lys Tyr Ser Ala Asp Phe Ile Gly Ile Gln Glu
272           500           505           510
273 Thr Arg Phe Leu Leu Ser Ala Met Glu Glu Arg Phe Pro Asp Leu Val
274           515           520           525
275 Lys Glu Cys Leu Arg Val Met Pro Val Gln Lys Ile Ala Glu Ile Leu
276           530           535           540
277 Gln Arg Leu Val Ser Glu Glu Val Ser Ile Arg Asn Leu Arg Ala Val
278           545           550           555           560
279 Leu Glu Ala Leu Val Glu Trp Gly Gln Lys Glu Lys Asp Thr Val Leu
280           565           570           575
281 Leu Thr Glu Tyr Val Arg Ile Ala Leu Lys Arg Tyr Ile Ser His Lys
282           580           585           590
283 Tyr Thr Ser Gly His Asn Ile Leu Pro Ala Tyr Leu Leu Ala Pro Lys
284           595           600           605
285 Val Glu Glu Thr Val Arg Ala Ala Ile Arg Gln Thr Ala Ala Gly Ser
286           610           615           620
287 Tyr Leu Ala Leu Asp Pro Asp Thr Thr Arg Arg Leu Val Glu His Ile
288           625           630           635           640
289 Arg Gln Cys Val Gly Asp Leu Ala Ala Gly Ala Ser Arg Pro Val Leu
290           645           650           655
291 Leu Thr Ser Met Asp Ile Arg Arg Tyr Thr Arg Lys Met Ile Glu Ala
292           660           665           670
293 Asp Leu Tyr Ala Leu Pro Val Leu Ser Tyr Gln Glu Leu Thr Pro Glu
294           675           680           685
295 Ile Asn Val Gln Pro Leu Gly Arg Val Asp Leu
296           690           695
298 <210> SEQ ID NO: 3

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VERIFICATION SUMMARY

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Output Set: N:\CRF3\07032001\I868604.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date